

**CLAIM AMENDMENTS**

This listing of claims will replace all prior versions, and listings, of claims in the application.

Claims 1-37 – cancelled.

38. (presently amended) A method to identify a test compound that modulates chromatin remodeling of a specific DNA sequence within chromatin comprising:
- a) providing one or more subunits of a SWI/SNF chromatin remodeling complex associated with a domain of a nucleic acid regulator protein;
  - b) contacting the one or more subunits of the chromatin remodeling complex associated with the domain of the nucleic acid regulator protein with the test compound; and
  - c) determining whether there is an increase or decrease in the interaction between the one or more subunits of the chromatin remodeling complex and the domain of the nucleic acid regulator protein, wherein an increase or decrease indicates that the compound modulates the chromatin remodeling of a specific DNA sequence with chromatin.
39. (previously presented) The method of claim 38, wherein the domain is a DNA binding domain.
40. (previously presented) The method of claim 38, wherein the nucleic acid regulatory protein is a transcription factor.
41. (previously presented) The method of claim 39, wherein the domain is a zinc-finger domain.
42. (presently amended) The method of claim 39, wherein the domain is helix-turn-helix or helix loop helix containing a leucine zipper motif motif.

43. (previously presented) The method of claim 38, wherein the domain is a peptide.

44. (cancelled)

45. (presently amended) ~~The method of claim 38, wherein the chromatin remodeling complex is A method to identify a test compound that modulates chromatin remodeling of a specific DNA sequence within chromatin comprising:~~

a) providing one or more subunits of a ISWI chromatin remodeling complex associated with a domain of a nucleic acid regulator protein;

b) contacting the one or more subunits of the chromatin remodeling complex associated with the domain of the nucleic acid regulatory protein with the test compound; and

c) determining whether there is an increase or decrease in the interaction between the one or more subunits of the chromatin remodeling complex and the domain of the nucleic acid regulatory protein, wherein an increase or decrease indicates that the compound modulates the chromatin remodeling of a specific DNA sequence with chromatin.

46. (presently amended) The method of claim 38 [[44]], wherein SWI/SNF complex is E-RC1.

47. (presently amended) The method of claim 38 [[44]], wherein the SWI/SNF complex is BRM.

48. (presently amended) The method of claim 38 [[44]], wherein the chromatin remodeling complex comprises BRG1.

49. (presently amended) The method of claim 38 [[44]], wherein the chromatin remodeling complex comprises BAF 155.

50. (presently amended) The method of claim 38 [[44]], wherein the chromatin remodeling complex comprises is BAF 170.
51. (presently amended) The method of claim 38 [[44]], wherein the chromatin remodeling complex comprises BRG1 and BAF 155.
52. (cancelled)
53. (previously presented) The method of claim 38, wherein the one or more subunits of the chromatin remodeling complex are selected from the group consisting of BRG1, BRM, BAF 155, BAF 170, INI1, BAF 60, BAF 47 and BAF 57.
54. (presently amended) The method of claim 38 or 45, wherein the nucleic acid regulatory protein is selected from the group consisting of GATA-1 , Spl , EKLF, FKLF, BKLF, GKLF, LKLF, Wilm's tumor suppressor protein (WT1), BRCA1, BRCA2, KRAB, BTB/POZ, Zif268, GLI, Xfin, a BTB/POZ domain containing zinc finger protein, PLZF (promyelocytic leukemia zinc finger) and a nuclear hormone receptor.
55. (presently amended) The method of claim 41 or 91, wherein the zinc finger domain is from a nuclear hormone receptor.
56. (previously presented) The method of claim 55, wherein the nuclear hormone receptor is selected from the group consisting of an androgen, estrogen, thyroid, progesterone, and glucocorticoid receptor.
57. (presently amended) The method of claim 38 or 45, wherein the nucleic acid regulatory protein binds to a promoter, an enhancer, an insulator, a silencer or locus of control regions (LCRs)].

58. (presently amended) The method of claim 38 or 45, wherein one or more subunits of the chromatin remodeling complex or the domain of a nucleic acid regulatory protein is labeled with a fluorescent tag.
59. (presently amended) The method of claim 38 or 45, further comprising using the test compound in an *in vitro* chromatin remodeling or transcription assay comprising the specific DNA sequence.
60. (presently amended) The method of claim 38 or 45, wherein the test compound is a small molecule.
61. (presently amended) The method of claim 38 or 45, wherein the test compound is a peptide.
62. (cancelled)
63. (presently amended) A method to identify a test compound that modulates chromatin remodeling of a specific DNA sequence within chromatin comprising:  
a) providing chromatin assembled DNA containing the specific DNA sequence;  
b) contacting the chromatin assembled DNA with one or more subunits of an SWI/SNF chromatin remodeling complex, a domain of a nucleic acid regulator protein; and  
c) determining the level of chromatin remodeling in the presence and absence of the test compound.
64. (previously presented) The method of claim 63, wherein the specific DNA sequence is an individual gene or portion thereof, a regulatory region or a chromosomal region.
65. (previously presented) The method of claim 63, wherein the domain is a DNA binding domain.

66. (previously presented) The method of claim 63, wherein the nucleic acid regulatory protein is a transcription factor.

67. (cancelled)

68. (presently amended) The method of claim 65, wherein the domain is helix-turn-helix or helix loop helix containing a leucine zipper motif ~~motif~~.

69. (previously presented) The method of claim 63, wherein the domain is a peptide.

70. (cancelled)

71. (presently amended) ~~The method of claim 63, wherein the chromatin remodeling complex is A method to identify a test compound that modulates chromatin remodeling of a specific DNA sequence within chromatin comprising:~~

a) providing chromatin assembled DNA containing the specific DNA sequence;

b) contacting the chromatin assembled DNA with one or more subunits of a

ISWI chromatin remodeling complex, a domain of a nucleic acid regulatory protein, and the test compound; and

c) determining the level of chromatin remodeling in the presence and absence of the test compound.

72. (presently amended) The method of claim 63 [[70]], wherein the SWI/SNF complex is E-RC1.

73. (presently amended) The method of claim 63 [[70]], wherein the SWI/SNF complex is BRM.

74. (presently amended) The method of claim 63 [[70]], wherein the chromatin remodeling complex comprises BRG1.

75. (presently amended) The method of claim 63 [[70]], wherein the chromatin remodeling complex comprises BAF 155.
76. (presently amended) The method of claim 63 [[70]], wherein the chromatin remodeling complex comprises BAF 170.
77. (presently amended) The method of claim 63 [[70]], wherein the chromatin remodeling complex comprises BRG1 and BAF 155.
78. (cancelled)
79. (presently amended) The method of claim 63 [[70]], wherein the one or more subunits of a chromatin remodeling complex are selected from the group consisting of BRG1, BRM, BAF 155, BAF 170, INI1, BAF 60, BAF 47 and BAF 57.
80. (presently amended) The method of claim 63 or 71, wherein the nucleic acid regulatory protein is selected from the group consisting of GATA-1, Sp1, EKLF, FKLF, BKLF, GKLF, LKLF, Wilm's tumor suppressor protein (WT1), BRCA1, BRCA2, KRAB, BTB/POZ, Zif268, GLI, Xfin, a BTB/POZ domain containing zinc finger protein, PLZF (promyelocytic leukemia zinc finger) and a nuclear hormone receptor.
81. (presently amended) The method of claim 63 or 71, wherein the domain is from a nuclear hormone receptor.
82. (previously presented) The method of claim 81, wherein the nuclear hormone receptor is selected from the group consisting of an androgen, estrogen, thyroid, progesterone, and glucocorticoid receptor.
83. (presently amended) The method of claim 63 or 71, wherein the nucleic acid regulatory protein binds to a promoter, an enhancer, an insulator, a silencer or locus of control regions (LCRs)).

84. (presently amended) The method of claim 63 or 71, the test compound is a small molecule.
85. (presently amended) The method of claim 63 or 71, wherein the test compound is a peptide.
86. (cancelled)
87. (presently amended) The method of claim 63 or 71, further comprising using the test compound in an *in vitro* transcription assay comprising the specific DNA sequence.
88. (presently amended) The method of claim 63 or 71, wherein the amount of chromatin remodeling is determined by assaying for DNase hypersensitive sites within the specific DNA sequence.
89. (new) The new method of claim 45, wherein the domain is a DNA binding domain.
90. (new) The method of claim 45, wherein the nucleic acid regulatory protein is a transcription factor.
91. (new) The method of claim 45, wherein the domain is a zinc-finger domain.
92. (new) The method of claim 45, wherein the domain is helix-turn-helix or helix-loop-helix containing a leucine zipper motif.
93. (new) The method of claim 45, wherein the domain is a peptide.
94. (new) The method of claim 71, wherein the specific DNA sequence is an individual gene or portion thereof, a regulatory region or a chromosomal region.

95. (new) , The method of claim 71, wherein the domain is a DNA binding domain.

96. (new) The method of claim 71, wherein the nucleic acid regulatory protein is a transcription factor.

97. (new) The method of claim 71, wherein the domain is a zinc-finger domain.

98. (new) The method of claim 71, wherein the domain is helix-turn-helix or helix loop helix containing a leucine zipper motif.

99. (new) The method of claim 71, wherein the domain is a peptide.